

Remarks

Applicants have been requested to correct drawings Figs. 1 – 8. As described below, the specification has been amended to comply with the correction. No new matter has been added by this Amendment.

The Official Draftsperson has indicated that views are not labeled properly in Figs. 2-5, 7 and 8. The drawings have been corrected and the specification has been amended to correspond with number changes and matters of form as it pertains to 2A-2B, 3A-3B, 4A-4B, 5A-5B, 7A-7B and 8A-8B.

In addition, lines in Fig. 6 have been changed to make them more uniformly thick and well defined.

Numbers and reference characters in all of the drawings have been made more plain and legible.

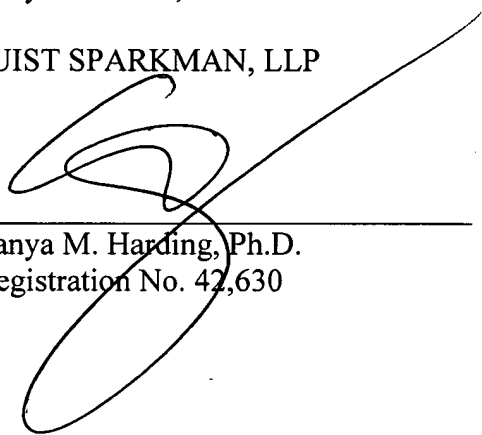
Conclusions

It is believed that this Amendment fully addresses the requested corrections in the Notice Regarding Drawings. Applicants therefore respectfully request that a patent issue in this case. The Official Draftsperson is requested to telephone the undersigned at the number listed below if it may expedite the issuance of the patent.

Respectfully submitted,

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By



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WO 01/1106:

CT/CA00/00907

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Figure 1. *Arabidopsis thaliana* *FAE1* promoter:
(Length: 934 bp)

-950 ACTCA TAAAACTAG TAGATTGGTT GGTGGTTTC CATGTACCAG
AtproFW →
-900 AAGGCTTACC CTATTAGTTG AAAGTTGAAA CTTTGTCCC TACTCAATTC
-850 CTAGTTGTGT AAATGTATGT ATATGTAATG CGTATAAAC GTAGTACTTA
-800 AATGACTAGG AGTGGTTCTT GAGACCGATG AGAGATGGGA GCAGAACTAA
-750 AGATGATGAC ATAATTAAGA ACGAATTGA AAGGCTCTTA GGTTTGAATC
-700 CTATTCGAGA ATGTTTTTGT CAAAGATAGT GGCGATTTTG AACCAAAGAA
-650 AACATTTAAA AAATCAGTAT CCGTTACGT TCATGCAAAT AGAAAGTGGT
-600 CTAGGATCTG ATTGTAATTT TAGACTTAAA GAGTCTCTTA AGATTCAATC
-550 CTGGCTGTGT ACAAACTAC AAATAATATA TTTTAGACTA TTTGGCCTTA
-500 ACTAACTTC CACTCATTAT TTAAGGAGT TAGAGAATAG ACTTGCGAAT
-450 AAACACATTC CCGAGAAATA CTCATGATCC CATAATTAGT CAGAGGGTAT
-400 GCCAATCAGA TCTAAGAACA CACATCCCT CAAATTTTAA TGCACATGTA
-350 ATCATAGTTT AGCACAATTC AAAAATAATG TAGTATTAAA GACAGAAATT
-300 TGTAGACTTT TTTTGGCGT TAAAGGAAGA CTAAGTTTAT ACGTACATTT
-250 TATTTTAAGT GGAAAACCGA AATTTCCAT CGAAATATAT GAATTTAGTA
-200 TATATATTTT TGCAATGTAC TATTTTGCTA TTTGGCAAC TTTCAGTGGA
-150 CTACTACTTT ATTACAATGT GTATGGATGC ATGAGTTTGA GTATACACAT
-100 GTCTAAATGC ATGCTTTGCA AAACGTAACG GACCACAAA GAGGATCCAT
-50 GCAAATACAT CTCATAGCTT CCTCCATTAT TTTCCGACAC AAACAGAGCA
← AtproRV
1 ATGACGTCCG TTAACGTAA GCTCCTT

FIG. 1

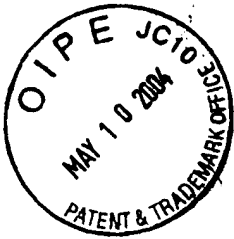
A circular stamp from the Office of Intellectual Property (OIP). The text "OIP" is at the top, "JC10" is at the top right, "MAY 10 2004" is in the center, and "PATENT & TRADEMARK OFFICE" is at the bottom.

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***Brassica napus* FAE1 promoter:**
(Length: 1588 bp)

FIG. 2A

315



(Continued)

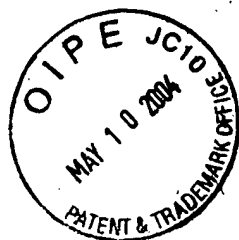
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-450 GTTACATAGA TTTGGAAACA CTTTCATCTAG CTCATATGG TATGAGTTGG
-400 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
-350 ATTGCTTTAG GGTCAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
-300 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
-250 GATACCCGGT CAAAATTGAT TCTGATTCAG GTAAGTCAGA GACTCGTGTC
-200 CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
-150 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
-100 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGTATC
-50 TCTTATTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCCG
      ← BnproRV
  1  ATGACGTCCA TTAACGTAAA GCTCCTTTAC CATTACGTCA TAACCAACCT
      ← Bnwalk2
  51 TTTCAACCTT TGCTTCTTTC CGTTAACGGC GATCGTCGCC GGAAAAGCCT
      ← Bnwalk1
 101 ATCGGCTTAC CATAGACGAT CTTCAACCACT TATACTATTC CTATCTCCAA
 151 CACAACCTCA TAACCATCGC TCCACTCTTT GCCTTCACCG

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FIG. 2B

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Figure 3. *Lunaria annua* FAE1 promoter:
(Length: 1069 bp)

```
-1100          CG CCGGGGAGTT TCAGCTTAAC CGGTAAAATT
                                     LaproFW →
-1050 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
-1000 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATAAA
-950  GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
-900  TGGCCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
-850  GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
-800  TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
-750  AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
-700  AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
-650  ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
-600  TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
-550  TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
-500  AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
-450  CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
-400  TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
-350  ATAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
-300  TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTTTATA
-250  TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
-200  TATTAATTAA TATTTTTTTA ATCGGACTAC TTTCTATTT TGGCACCTTT
-150  CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA
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F16.3A

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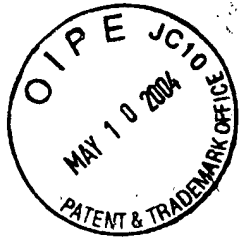
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-100 ATACACATGT CTATATAAAT GCATGTAAAA CGTAACGGAC CACAAAAGTG
-50 GATCCATACA AATACATCTC ATCGCACCTT CTCCGACACA AAACTGAACA
                                     ← LaprovR
  1 ATGACGTCTG TGAACGTAA ACTCCTTTAC CATTACGTCA TAACCAACTT
51 TTTCAACCTC TGTTTCTTCC CACTGACGGG GATCCTCGCC GGAAAAGGCT
                                     ← Lawalk2
101 CTCGTCTTAC CACAAACGAT CTCCACCA
                                     ← Lawalk1

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FIG. 3B

6115



CLUSTAL W (1.74) multiple sequence alignment

[illegible]

FIG. 4A

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~~Figure 4 Continued~~ Alignment of A.t., L.a. and B.n. FAE1 promoters (continued)

A.t. TTGGTTTCCA--TGTACCAGAAGGCTTACCCTAT-TAGTTGAAAGTTGAACTTTGTTC
L.a. TTGTTACTCAATTGGGCTAAGTGTATTATTATAT-GTGTGTATATAATAAGGTAGAAC
B.n. ACTTGTGCATGTCCATAAAATACGTATGCTCTTGTGGTGAGCACAGAGAACATCACTT
* * * * *
Con. 4 WYKKWYBCANNTSBRYHARRWKDMKTAYBMTMTNKWGKTGWRHRYWRWRAMBDTVDHHY

A.t. CTAATCAATTCCTAGTTGTGTAAATGT---ATGTATATGTAAT---GCGTATAAAACGTA
L.a. GTAA--ATTACTAAGAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTG
B.n. ATAA-CATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCGCTGTT
* * * * *
Con. 4 VTAMNNAWTTMCMMDKDDKRTRWWWKNNNATGWDDDTKYHMWNNGCBTVTMVRYKTD

A.t. GTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGAGATGGGAG-CAGAATAAAG
L.a. AATCCTACTCGAGAAG-ACTAATTTTAATTTACTGGCAAAATAGAAA-TCAATTTATAA
B.n. GGTGGGGC-CGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGCGGTCCAAGTACGA
* * * * *
Con. 4 RDWSBKRMNYGMBWWKNWSYDVITYWWVDDMCKRKVRRWVRTRGRMRNYMVABTAHRR

A.t. AT--GATGACATAATTA-----AGAACGAATTTGA-AAGG-CTCTTAGGTTTGAATCCT
L.a. GT--GTTTAAACAAATCGATGGTATAACTGATTAGT-GATCACTCTTAGGTTTGTATCCA
B.n. GCTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCA
* * * * *
Con. 4 RYNNGWTBAMAYRRWTMNNNNNNNAKAMCKRAKYWGNRABVNSTCTTWKSKTTKVRTSCW

A.t. ATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAAAGAAAACATTTAAA-A
L.a. ACTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAAAATCTTGATTTTAA-A
B.n. A--CAAGGA-GACGATGAGAACGGCAA----AATCGGAGTGAGTTTGTCCAAGGACATA
* * * * *
Con. 4 ANNCRAGDANKDHKWKWSAAMGVYWNNNNNNNNTYKKARHBARWDVWWSAWKKWHANA

A.t. AATCAGTATCCGGTTAC---GTTTCATGCAAATAGAAAGTGGTCTA---GGATCTGATT-
L.a. ATTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTTCTCTTTGTTTAAATGGGTTTGTGTT-
B.n. ACCGATGTTGCTGGTGAACGGTTAAGAAAAACATAGCAACGTT----GGGTCGGTTGA
* * * * *
Con. 4 AHYSRKKWTBYKRKTVMNNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKN

A.t. GTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGCT-GTGTACAAAAC
L.a. TGCATTTTATAAGCTTAATTTTTCTAATTTAATATTTTATCTATCATCGTCCGTAAAGTT
B.n. TTCTTCGGTTAAGCGAGAACTTCTT--TTTTTCGTTA--CCTTCATGGGCAAGAACTT
* * * * *
Con. 4 KKMWTYYKWKANNCKWRAWDHKTCTHNNTTWWMKTYWNNCYWKSMTNGKSHRBAAAVYT

A.t. ACAAATAATATA----TTTTAGACTATTTGGCCTTAATAAACTTCCA-CTCATTATTTA
L.a. TTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGGGAAGTGGTTGAGT-
B.n. TTCAAAGATAAAATCAAACATTACTACGTCCTCGGATTTCAAACCTTGCTATTGACCATTT
* * * * *
Con. 4 WYMWWRRYAHANNNNWDYWWKACTWYKYBVCSSKWWNNYAAWYTKSSWNYTSRYRWKTN

A.t. -CTGAGGTTAGAGAA--TAGACTTGCGAATAAACACATTCCTCGAGAAATACTCATGATCC
L.a. -CAAAGCGTACCGGA--CAAATATGTTT-TATATTCTTATTTAAGAATTAACACTCATCT
B.n. TGTATACATGCCGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCA
* * * * *
Con. 4 NSWRWRS DTRSMGRANNYARABHYGYKNTRWVBWSHTWBHBRAGAAYWMBMMYBAKCH

Fig. 4B

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Figure 4 Continued: Alignment of A.t., L.a. and B.n. FAEl promoters

(continued)

CE3

```

A.t.      CATAATTAGTCAGAGGGTATG-----CCAATCAGATCTAAGAACACACATTCCCTC
L.a.      CATAATTAGTCAGAGGCTAGGGAGATTCAGCCAATCAATGCTAACAAACA-ATTCTCTT
B.n.      CCGATCGATGTAGAGGC-----ATCAAGATCAACGTTACATAGATTGG
          * * * * * * * * * * * * * * * * * * * *
Con. 4    CMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNNNNATCARDYYAASRWYAMANAKWYYKYB

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```

A.t.      AA--ATTTTA--ATGCAC-ATGTAATCAT-----AGTTT-----AGCACAATTCAAAA
L.a.      AATGATCTAACGATGCT--ATTTAATATTCGGATCAGTATCTCTAAATAAGAATATAAAA
B.n.      AAACACTTCATCTAGCTCAATATGGTATG-----AGTTGGCATACAT-AGAAG-CAAAA
          * * * * *
Con. 4    AANNAYYTHANNWWGCWNNATDTRRTMWKNNNNNNNAGTWKNNNNNNNAKNASAAKNYAAAA

```

A. t. ATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT---TTGGCGT-TAAAGG
L. a. CTAATTCAATAGTTACAGATAAAACCTTATATAGACTTTTTTAT--TTGGAATATAAAAG
B. n. GGAAGGATGAA-GAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTAAAGT
* * * * *
Con. 4 VKAAKKHWRWANKWAMRGWHADAAABTTDKRNNGAYTKYTTNNNNNTYRGVVTNTAARDG

A.t. AA-----GACTAAGTTTATA-CGT-----ACATTT-TATTTTAAGT
L.a. TATCAATATATTATA-GACAATATTTTATAACGTTAAAAATACAATATTTTATATTTTTTAT
B.n. TAACAGTCGAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCCTTGGGA
* * * * *
Con. 4 WANNNNNNNNNNNNNNNGWSDMVWTWWAYANYGTNNNNNNNNNNNAYAWWTNKWYYTTDDR

CE1

A.t. GGA-----AAACCGAAATT--TTCCATCGAAATATATGA--ATTT-AGTATAT-----
L.a. ATATTTATTTCAAATTGAAAGCATTACTTCTATCGAAATGA--ATTTTAGTATATTAAT
B.n. ACAC-----GCATCGACAGATACCCGGTCAAATTGATTCTGATTCAAGGTAAAGTCAGA
* * * * *
Con. 4 RBAYTNNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDA TKMNNATTYNRGTAWRTNNNN

G-box2

```

A. t.      --ATATTTCTGCAAT-----GTACTATTTTGCTATTTTGGCAA-CTTTTCAGTGGACTAC
L. a.      TAATATTTTTTTTAATC-----GGACTACTTTCCTATTTTGGCAC-CTTTTCATCTGACTAC
B. n.      GACTCGTGTGCCAAACGGTCGGCTCTAATAAACGATGTTTGCCTCTCTCTTCGTTT-----CTTT
           * * * * *
Con. 4     NNMTMKTKYYBHAAWNNNNNNGKMCTAHTWWVCKATKTTKGCMNCTTTCKRYKNNCTWY

```

G-box1

```

A.t.      TACTTTATTACAATGTGT--ATGGATGC-ATGAG---TTTGAGTA-TACACATGTCCTAAA
L.a.      TAATTTATTTCAATGTGT--ATGCATGC-ATGAG---CATGAGTAATACACATGTCCTATA
B.n.      TTATTTGTTATAATAATTTGATGGCTACGATGTTCTCTTGTTGTTATGAATAAAGAAT
          *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
Con. 4    TWMITTRTTWYAATRWKTNNAATGSMTRCNATGWKNNNYWTGWKTRWTAAYRMATRWMKAWW

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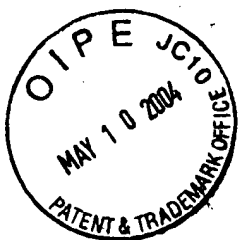
A-300 EM1 ABA

A. t. TGCATGCT-TTGCAAAACGTAACGGACC-ACAAAAGAGGATCCATTGCAAAATACATCTCAT
L. a. TAAATGCA-T-GTAAACGTAACGGACC-ACAAAAGTGGATCCATACAAATACATCTCAT
B. n. GCAATGGTGTTCTAGTATTGGATTGTTTACATGTATGTATCTCTT-ATTTACATGAAAT
*** * * * *
Con. 4 KVMATGSWNTNSYARWAYKTRAYKGWYYNACAWRWRWGKATCYMTDNAWWTACATSWMAT

A. t. AGC-TTCCTCCATTATTTTCCGACACAAA-CAGAGCA---
 L. a. CGC-ACCTC-----TCCGACACAAAAGTGAACA---
 B. n. TTTTAAACGCC-----TAAAAAAGCAACGGAAATCCG
 * * * * * *
 Con. 4 HKYNWHMCKCNNNNNNNTMMRAMAMAAANCDGARYWNNN

FIG. 4C

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CLUSTAL W (1.74) multiple sequence alignment

-400

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~~Figure 5 Continued:~~ Alignment of *A.t.* and *L.a.* *FAE1* promoters (continued)

A.t.	-381	CACATTCCCTCAA--ATTTTA--ATGCACATGTAATCAT-----AGTTT-----AGCA
L.a.		AA-ATTCTCTTAATGATCTAACGATGCT-ATTTAATATTCGGATCAGTATTCTTAAATAA
		* * * * *
Con.5		MANATTCTCYTYAANNATYTWANNATGCWNATKTAATMWTNNNNNNNAGTWTNNNNNNNAKMA
A.t.	-337	CAATTCAAAAATAATGTAGTA-TTAAAGACAGAAATTGTA--GACTTTTTT--TTGGCG
L.a.		GAATATAAACTAATTCAATAGTTACAGATAAAACTTATATAGACTTTTTTATTGGAA
		* * * * *
Con.5		SAATWYAAAAMTAATKYARTANTTAMAGAYARAAAYTTRTANNGACTTTTTTNNTTGGMR
A.t.	-282	T-TAAAGGAA-----GACTAAGTTTATA-CGT-----ACATTT-TAT
L.a.		TATAAAGTATCAATATATTATAGACAATATTTATAACGTTAAAAATACAATATTATAT
		* * * * *
Con.5		TNTAAARGWANNNNNNNNNNNGACWAWRTTTATANCGTNNNNNNNNNNAYATTTNTAT
A.t.	-247	TTTAAGTGGA-----AAACCGAAATT--TTCCATCGAAATATATGAATTT-AGTATA
L.a.		TTTTTATATATTTATTCAAATTGAAAAGCATTACTTCTATCGAAATGAATTTTAGTATA
		* * * * *
Con.5		TTTWWRTRKANNNNNNNNNAAAYYGAAWKNNTTMCWTCKAWMKAWATGAATTTNAGTATA
A.t.	-198	T-----ATATTTCTGCAAT-GTACTATTTTGCTATTTTGGCACTTTTCAGTGGACTACT
L.a.		TTAATTAATATTTTTTAAATCGGACTACTTTCTATTTTGGCACCTTTCATCTGACTACT
		* * * * *
Con.5		TNNNNNNATATTTYTKYAATNGKACTAYTTTCTATTTTGGCAMCTTTCAYKKGACTACT
A.t.	-145	ACTTTATTACAATGTGTATGGATGCATGAGTTTGAGTA-TACACATGTCTAAATGCATGC
L.a.		AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATACACATGTCTATATAAATGC
		* * * * *
Con.5		AMTTTATTWCAATGTGTATGSATGCATGAGYWTGAGTANTACACATGTCTAWATRMATGC
A.t.	-86	TTTGCAAAACGTAACGGACCACAAAAGAGGATCCATGCAAATACATCTCATAGCTTCCTC
L.a.		AT-GTAAACGTAACGGACCACAAAAGTGGATCCATACAAATACATCTCATCGCACCTC
		* * * * *
Con.5		WTNGYAAAACGTAACGGACCACAAAAGWGATCCATRCAAATACATCTCATMGCWYCCTC
A.t.	-26	CATTATTTTCCGACACAAA-CAGAGCA
L.a.		-----TCCGACACAAAAGTGAACA
		* * * * *
Con.5		NNNNNNNTCCGACACAAANCWGARCA

FIG. 5B



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Figure 6

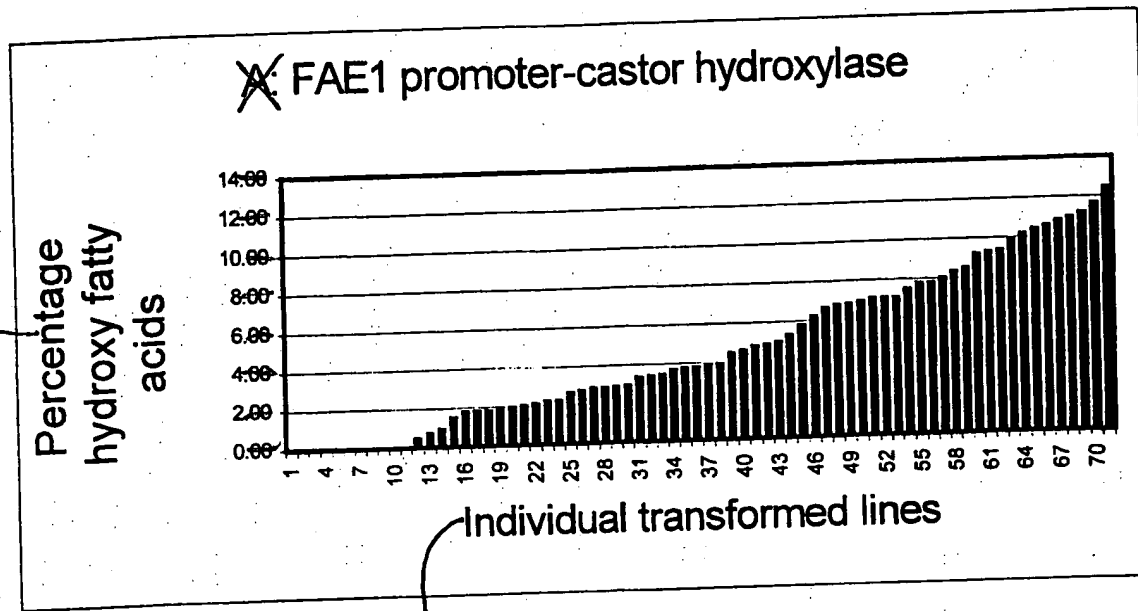


FIG. 6A

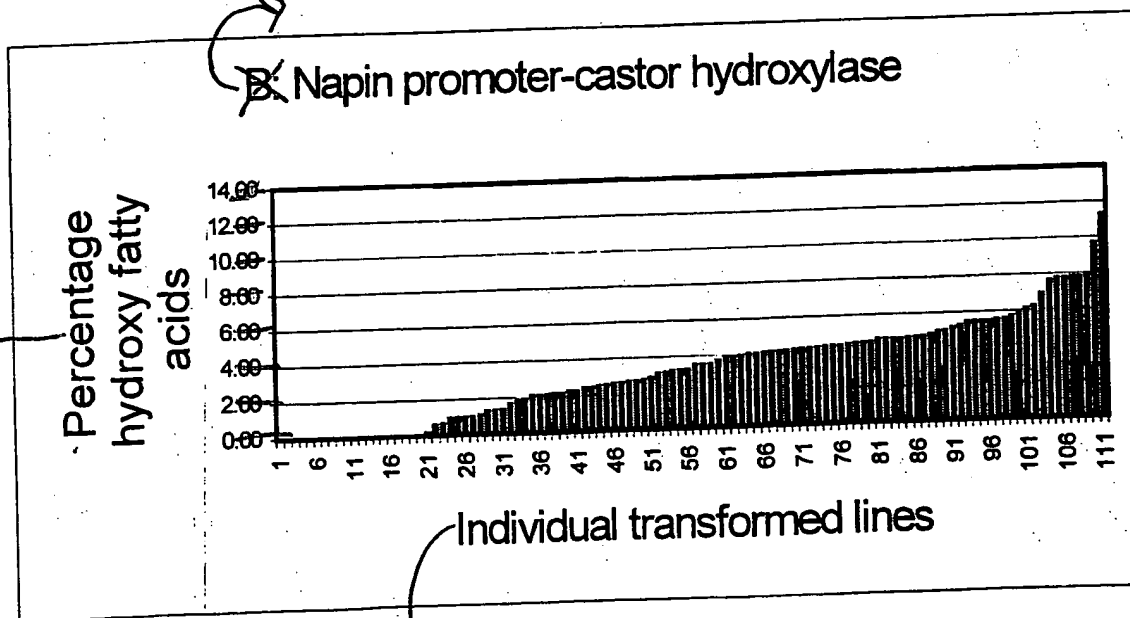


FIG. 6B

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~~Figure 7:~~ Alignment of *B.n.* and *L.a.* *FAE1* promoters

CLUSTAL W (1.81) multiple sequence alignment

```
BnFAE1      GGTGGGCAAATCTGACTTCACCAAAGAAACAACTCGAGTCGTTATCCATCTCCTCATAA 60
LaFAE1      -----

BnFAE1      CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCTCTACATCGCAACCCGGC 120
LaFAE1      -----

BnFAE1      CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180
LaFAE1      -----CGCCGGGGAGT-TCAGCTTAACCGGTAAAATTGGCCTGTACATATA 46
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
LaFAE1      TTTACCACTGAGT-AAAGACATCAGTTAATGATT-----GTTGTTACTCAATTGGGCT 99
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTCAAGGTC 300
LaFAE1      AAGTGTATTATTATATGTGTG-----TATATAATAAAGGT---AGAACGT---AAATT 147
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      TAGGCGATGAAACTCACGGGCCGAGGGGCTGCTTCAGGTCCCTCCCGGAAGACTTTTG 360
LaFAE1      TA--CTAAGATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTGAATCCTA 205
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CGGCGGCGCGTGAAGAGACGGAGCAAGTTATCATTGGTGCGCTAGAAAATCTATTCAAGA 420
LaFAE1      CT-----CGAGAAGACTAATTTTAAT-TTACTGGCAAAAATAGAAATCAATTTATAA 256
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      ACACCAACGTTAACCCTAAAGATATAGGTATACTTGTGGTGAAGTCAAGCATGTTTAAATC 480
LaFAE1      GTGTTTAAACAAATC--GATGGTATAACTG-ATTAGTGATCACTCTTAGGTT--TTGATC 311
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CAACTCCATCGCTCTCCGCGATGGTCGTTAACAACCTTTCAAGCTCCGAAGCAACGTAAGAA 540
LaFAE1      CAACTCGAGTATTG-----AGTATTGAACGCTTT-----TTTTAAATAAAATCTTGA 358
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGCGCTTATAGCCATTGATCTAGCAAAGG 600
LaFAE1      TTTTAAA-TTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTTCTCTT-TGTTTTAATGG 416
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      ACTTGTTCATGTCC-ATAAAAATACGSTATGCTCTTGTGGTGAGCACAGAGAACATCACT 659
LaFAE1      GTTTGTTTTGCATTTTATAAGCTTAATTTTCTAATTTAAT-ATTTTATCATCATCGTC 475
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTTCAAATTGCTTGTTCGGTGT 719
LaFAE1      CGTAAAGTTT-----TATTTGGCACAACTTGTTTTA---CTTTTCTACCTTATA 522
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      GGTGGGGCCGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGAG 779
LaFAE1      ATTTGGGA-ACTGGTTGAGTCA-----AAGCGTACCGGACAAATATGTTTATATTC--- 573
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCAA 839
LaFAE1      -TTATTTA-AGAATTAACACTCATCTCATAATTAGTCAGAGGC-----TAGGGAGATT 624
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1      CAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAACCGATGTT 899
LaFAE1      CAGCCAATCAATGCTAACAACAAATTTCTTTAA--TGATCTAACGATGCTATTTAATAT 682
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
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~~Figure 7 Continued~~: Alignment of *B.n.* and *L.a.* *FAE1* promoters

BnFAE1	GCTGGT CGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCCGTTA-AG	958
LaFAE1	TCGGATCAGTATTCTTAAATAAGAATATAAA-----ACTAATTCAATAGTTACAG	732
	* * * * *	
BnFAE1	CGAGAAACTTCTTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATAAAATCAA	1018
LaFAE1	ATAAAACTTATATAGACTTTTTTATTG-GAATATAAAAGTATCAATATATTATAGACA	791
	* * * * *	
BnFAE1	ACATTACTACGTCCCGGATTTCAAACCTTGCTATTGACCATTTTGTATACATGCCGGAGG	1078
LaFAE1	ATATTTATA-----ACGTTAAAAATACAATATTATATTTTATATATTTATTTCAAA	845
	* * * * *	
BnFAE1	CAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGTAGAGGC	1138
LaFAE1	TTGAAAAGCATTACTTCTATCGAAATGAATTTTAGT-----ATATTAATTAATATTTTTT	901
	* * * * *	
BnFAE1	ATCAAGATCAACGTTACATAGATTTGGAAACACTTCATCTAGCTCAATATGGTATGAGTT	1198
LaFAE1	AATCGGACTACTTTCCTAT-----TTTGGCACCTTCATCTGACT-----ACT	944
	* * * * *	
BnFAE1	GGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTT	1258
LaFAE1	AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATA-----CACATGTCTAT	996
	* * * * *	
BnFAE1	AGGGTCAGGCTTTAAGTGTAAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTC	1318
LaFAE1	ATAAATGCATGTAAACGTAACGG-ACCACAAAGTGGATCCATACAAATACATCTCATC	1055
	* * * * *	
BnFAE1	GACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAATGATTCTGATTC	1378
LaFAE1	G-CACCCCTCTCCGACACAAAACGAACA-----	1082
	* * * * *	
BnFAE1	AGGTAAGTCAGAGACTCGTGTCCAAACGGTCGGTCCTAATAAACGATGTTTGCTCTCTT	1438
LaFAE1	-----	
BnFAE1	TCGTTTCTTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTGTTTGTATG	1498
LaFAE1	-----	
BnFAE1	AATAAAGAATGCAATGGTGTCTAGTATTTGATTGTTTTACATGTATGTATCTCTTATT	1558
LaFAE1	-----	
BnFAE1	ACATGAAATTTTAAACGCCTAAAAAACAACCGAATTCCG	1600
LaFAE1	-----	

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Figure 8: Alignment of *B.n.* and *A.t.* *FAE1* promoters

CLUSTAL W (1.81) multiple sequence alignment

AtFAE1
BnFAE1

GGTTGGGCAAATCTGACTTCACCAAAGAAACAACTCGAGTCGTTATCCATCTCCTCATAA 60

AtFAE1
BnFAE1

CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCCTACATCGCAACCCGGC 120

AtFAE1
BnFAE1

CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180

AtFAE1
BnFAE1

-----ACTCATAAAA 10
GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
*** **

AtFAE1
BnFAE1

ACTAGTAGATTGGTTGGT--TGGTTTCCATGTACCAGAAGGCTT-----ACCCTATTAGT 63
GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAGAACGTTCCAGTGC 300
* ** * * * * * * * * * * * * * * *

AtFAE1
BnFAE1

TGAAAGTTGAAACTT-TGTTCCCTACT--CAATTCCTAGTTGTGTAAATGTATGTATATG 120
TAGGCGGATGAAACTCACGGGCCCCGAGGGGCTGTTTCAGGTCCCTCCCCGGAAGACTTTTG 360
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

TAATG-CGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTTCCTTGAGACCGATGAGAG 179
CGGCGGCGCGTGAAGAGACGGAGC-AAGTTATCATTGGTGCCTAGAAAATCTATTCAAG 419
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

A----TGGGAGCAGAACTAAAGATGATGACATAATTAAGAACGAATTTGAAAGGCTCTTA 235
AACACCAACGTTAACCTTAAAGATATAGGTATACTTGTGG-TGAACCTCAAGCATGTTTAA 478
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

GGTTTGAATCCTATTTCGAGAATGTTTTTGTCAAAGATAGTGGCGA-TTTGAACCAAAGA 294
---TCCAACCTCATCGCTCTCCGCGATGGTTCGTTAACACTTTCAGCTCCGAAGCAACGT 535
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

AAACATTTAAAAAATCAGTATCC--GGTTAC-GTTCATGCAA-ATAGAAAGTGGTCTAGG 350
AAGAAGCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGCGGTTATAGCCATTGATCTAGC 595
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ATCTGATTGTAATTTTAGACTTAAAGAGTCTCTTAAGATTCAATCCTGGCTGTGTACAAA 410
AAAGGACTT--GTTGCATGTCCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAAC 653
* ** * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ACTACAAATAATATAT---TTTAGACTATTTGGCCTTAACTAAACTTCCACTCATTATTT 467
ATCACTTATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAATTGCTTGTTC 713
* ** * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ACTGAGGTTAGAGA-ATAGACTTGCGAATAAACACATTCCCGAGAAATACTCATGATCCC 526
CGTGTGTTGGTGGGGCCGCTATTTTGTCTCTCCAACAAG--CCTGGAGATCGTAGACGGTCCA 771
* * * * * * * * * * * * * * *

CE3

AtFAE1
BnFAE1

ATAATTAGTCAGAGGGTATG--CCAATCAGATCTAAGAACACACATTCCTCAATTTTA 584
AGTACGAGCTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTT 831
* * * * * * * * * * * * * * *

AtFAE1
BnFAE1

ATGCACATGTAATCATAGTTTAGCACAATTCAAAAATAATGTAGTATTAAAGACAGAAAT 644
GCGTGCAACAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAA 891



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Figure 8 Continued: Alignment of *B.n.* and *A.t.* *FAE1* promoters

AtFAE1	TTGTAGACTTTTTTTTGGCGTTAAAGGAAGACTAAG-----TTTATACGTACATTTTAT	698
BnFAE1	CCGATGTTGCTGGTCAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTC	951
	* * * * *	
AtFAE1	T-TTAAGTGGAAAACCGAAATTTTCCAT-----CGAAATATATGAATTAGTATATATA	751
BnFAE1	CGTTAAGCGAGAAACTTCTTTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATA	1011

	G box 2	
AtFAE1	TTTCTGCAATGTACTATTTTGCTATTTTGGCAACTTTCAGTGGACTACTACTTTAT-TAC	810
BnFAE1	AAATCAAACATTACTACGTCCCGGATTTC-AACTTGCTATTGACCATTTTGTATACAT	1070
	* * * * *	
	G-box 1	
AtFAE1	AATGTGTATGGATGCGATGAGTT-TGAGTATACACATGTCTAAATGCATGCTTTGCAAAAC	869
BnFAE1	GCCGGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCAGATCGAT	1130
	* * * * *	
AtFAE1	GTAACGG-ACCACAAAAGAGGATCCAT-----GCAAATACATCTCATAGCTTCTCTCCAT	922
BnFAE1	GTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGG	1190
	*** * * * *	
AtFAE1	TATTTTCCGACACAAACAGA-GCA-----	945
BnFAE1	TATGAGTTGGCATACATAGAAGCAAAGGAAGGATGAAGAAAGGTAATAAGTTTGGCAG	1250
	*** * * * *	
AtFAE1	-----	
BnFAE1	ATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTAAACAATGTC	1310

AtFAE1	-----	
BnFAE1	AAAGCTTCGACAAATAGTCCTTGGAACACTGCATCGACAGATACCCGGTCAAATTGAT	1370

AtFAE1	-----	
BnFAE1	TCTGATTCAGGTAAGTCAGAGACTCGTGTCCAAACGGTCGGTCCTAATAAACCAGTGT	1430

AtFAE1	-----	
BnFAE1	GCTCTCTTCGTTTCTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTTGT	1490

AtFAE1	-----	
BnFAE1	TTGTTATGAATAAAGAATGCAATGGTGTCTAGTATTGATTGTTTACATGTATGTATC	1550

AtFAE1	-----	
BnFAE1	TCTTATTTACATGAAATTTTAAACGCCTAAAAAAAACGGAATTCCG	1600

Fig. 8B

